

What is claimed is:

1. A method, comprising the steps of:
 - providing at least one peripheral blood sample of a human; and
 - comparing an expression profile of one or more genes in said at least one peripheral blood sample to at least one reference expression profile of said one or more genes, wherein each of said one or more genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having a solid tumor as compared to PBMCs of disease-free humans, provided that if said one or more genes consist of only one gene, said one gene is not selected from the group consisting of IL1B, IL6, MMP-9 and FCGR3B, and further provided that if said one or more genes consist of two genes, said two genes are not IL1B and IL6.
2. The method according to claim 1, wherein said solid tumor is selected from the group consisting of RCC, prostate cancer, and head/neck cancer.
3. The method according to claim 2, wherein said peripheral blood sample comprises enriched PBMCs.
4. The method according to claim 2, wherein, said peripheral blood sample is a whole blood sample.
5. The method according to claim 2, wherein the expression profile is determined using quantitative RT-PCR or an immunoassay.
6. The method according to claim 1, wherein said at least one reference expression profile comprises an expression profile of said one or more genes in peripheral blood samples of disease-free humans.
7. The method according to claim 6, wherein said at least one reference expression profile further comprises an expression profile of said one or more genes in peripheral blood samples of patients having said solid tumor.

8. The method according to claim 7, wherein said one or more genes include at least two genes, and the expression profile of the human is compared to said at least one reference expression profile using a weighted voting algorithm.

9. The method according to claim 6, wherein each of said one or more genes is differentially expressed in PBMCs of patients having another solid tumor relative to disease-free humans.

10. The method according to claim 9, wherein said solid tumor and said another solid tumor are different tumors selected from the group consisting of RCC, prostate cancer, and head/neck cancer.

11. The method according to claim 1, wherein said one or more genes include at least one gene selected from Table 4 or Table 6.

12. The method according to claim 1, wherein said one or more genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a classification probe sequence (CPS) selected from Table 2.

13. The method according to claim 1, wherein said one or more genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a qualifier selected from Attachment A.

14. The method according to claim 1, wherein said one or more genes include at least two genes selected from Table 4.

15. The method according to claim 1, wherein said one or more genes include a classifier identifiable using a two-class or multi-class correlation metric algorithm.

16. A method, comprising the steps of:
 providing at least one peripheral blood sample of a human having a non-blood disease; and
 comparing an expression profile of one or more genes in said at least one peripheral blood sample to at least one reference expression profile of said one or more

genes, wherein each of said one or more genes is differentially expressed in PBMCs of patients having the non-blood disease as compared to PBMCs of disease-free humans.

17. The method according to claim 16, wherein the non-blood disease is a solid tumor selected from the group consisting of RCC, prostate cancer, and head/neck cancer.

18. A method for identifying a gene which is differentially expressed in peripheral blood samples of non-blood disease patients as compared to peripheral blood samples of reference humans, comprising the steps of:

- providing an expression profile of one or more genes in peripheral blood samples of said non-blood disease patients;

- providing a reference expression profile of said one or more genes in peripheral blood samples of said reference humans; and

- comparing the expression profile to the reference expression profile to identify a gene that is differentially expressed in said non-blood disease patients relative to said reference humans.

19. A kit comprising:

- one or more polynucleotides, each of said one or more polynucleotides capable of hybridizing under stringent conditions to an RNA transcript, or the complement thereof, of a gene differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans; or

- one or more antibodies, each of said one or more antibodies capable of binding to a polypeptide encoded by a gene differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans.

20. A system comprising:

- a memory which stores at least one reference expression profile of one or more genes in peripheral blood samples of reference humans, wherein each of said one or more genes is differentially expressed in PBMCs of patients having a non-blood disease as compared to PBMCs of disease-free humans;

- a program capable of comparing an expression profile of interest to said at least one reference expression profile; and

- a processor capable of executing the program.